

XIANG Hua, HAN Jing, HOU Jing, ZHAO Dahe, CAI Shuangfeng and CAI Lei, 2014. Carbon Metabolism and Bioplastic Production by Halophilic Archaea. *Acta Geologica Sinica* (English Edition), 88(supp. 1): 116-118.

Carbon Metabolism and Bioplastic Production by Halophilic Archaea

XIANG Hua, HAN Jing, HOU Jing, ZHAO Dahe, CAI Shuangfeng and CAI Lei

Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China. Email: xiangh@im.ac.cn

1 Introduction

Haloarchaea represents a distinct group of Archaea that typically inhabits hypersaline environments, such as salt lakes and sea salterns. They are easy to culture and many haloarchaea are genetically tractable, hence they are excellent model systems for research of archaeal genetics, metabolism, and environmental adaptation. Furthermore, haloarchaea are capable of biosynthesis of extracellular polysaccharide, polyhydroxyalkanoates (PHA), bacteriorhodopsin, carotenoids and halophilic enzymes, etc., thus also have considerable biotechnological potentials. In the past a few years, we have systematically studied the carbon metabolism and PHA biosynthesis in haloarchaea, mainly with *Haloferax mediterranei* as a promising haloarchaeal cell factory (Fig.1).

2 Results and discussion

The *H. mediterranei* is a metabolically-versatile haloarchaeon, which is capable of biosynthesis of poly (3-hydroxybutyrate-co-3-hydroxyvalerate) (PHBV), a desirable bioplastic among PHAs, from unrelated carbon sources including some inexpensive raw materials, like starch, extruded rice bran and whey. Therefore, we have shown great interests in the carbon metabolism of this haloarchaeon, including sugar transportation (Cai *et al.*, 2014), chitin catabolism (Hou *et al.*, 2013b), and especially, the PHBV biosynthesis pathway (Han *et al.*, 2013) as well as the genome-wide regulation of PHA production (Liu *et al.*, 2013). These studies were greatly facilitated by the

availability of the genome sequences of the haloarchaea (Han *et al.*, 2012; Liu *et al.*, 2011b) and their highly efficient gene knockout systems (Liu *et al.*, 2011a).

Briefly, we have demonstrated that *H. mediterranei* biosynthesizes PHBV from acetyl-CoA and propionyl-CoA via a three-step process catalyzed by β -ketothiolase (PhaA/BktB), β -ketoacyl-CoA reductase (PhaB1/PhaB2), and PHA synthase (PhaEC) sequentially, with novel enzymes we identified for the first time in haloarchaea (Table 1). Notably, the two β -ketothiolases (PhaA and BktB) with different substrate specificities are distinct in both subunit composition and catalytic residues from bacterial PhaA/BktB (Hou *et al.*, 2013a). Two β -ketoacyl-CoA reductases, designated as PhaB1 and PhaB2 respectively, have also been identified to supply monomers for PHBV synthesis, of which PhaB2 is the major reductase (Feng *et al.*, 2010). As for the PHA

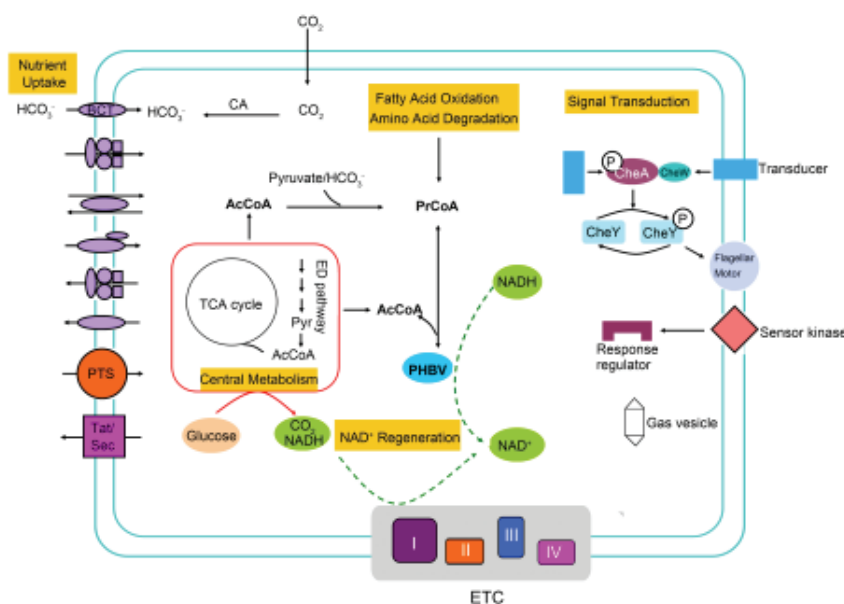


Fig. 1. An integrated view of carbon metabolism and PHBV biosynthesis in *Haloferax mediterranei*.

* Corresponding author. E-mail: xiangh@im.ac.cn

Table 1 Genes involved in PHBV synthesis by *H. mediterranei*

Enzyme/Protein	Gene	HFX ID	Reference
PhaA and BktB	<i>phaAα</i>	HFX_1023	Hou <i>et al.</i> , 2013a
	<i>phaAβ</i>	HFX_1022	
	<i>bktBa</i>	HFX_6004	
	<i>bktBβ</i>	HFX_6003	
PhaB1 and PhaB2	<i>phaB1</i>	HFX_1281	Han <i>et al.</i> , 2009; Feng <i>et al.</i> , 2010
	<i>phaB2</i>	HFX_5215	
PHA synthase	<i>phaE</i>	HFX_5220	Han <i>et al.</i> , 2007; Lu <i>et al.</i> , 2008; Han <i>et al.</i> , 2010a; Han <i>et al.</i> , 2010b
	<i>phaC</i>	HFX_5221	
	<i>phaC1</i>	HFX_2678	
	<i>phaC2</i>	HFX_6061	
	<i>phaC3</i>	HFX_6429	
Phasin	<i>phaP</i>	HFX_5219	Cai <i>et al.</i> , 2012

synthase, a novel archaeal subtype (IIIA) of type III PHA synthase represented by the one composed of PhaE_{Hme} and PhaC_{Hme} has been proposed, which is distinguished from bacterial subtype (IIIB) and widely distributed in haloarchaea (Lu *et al.*, 2008; Han *et al.*, 2010a). Additionally, three cryptic *phaC* genes have been identified in the genome of *H. mediterranei* (Han *et al.*, 2010b). In addition to the key enzymes, the PHA granule-associated protein of PhaP has also been revealed to be closely related with the PHBV granule formation. Notably, the PhaP protein of *H. mediterranei* shows no homology with bacterial PhaPs (Cai *et al.* 2012).

Significantly, four propionyl-CoA supplying pathways have been revealed to produce propionyl-CoA for PHBV synthesis in *H. mediterranei*, including two novel and major pathways, named citramalate/2-oxobutyrate pathway and 3-hydroxypropionate pathway, respectively (Han *et al.*, 2013). This 3-hydroxypropionate pathway, coupling CO₂ assimilation with biopolymer accumulation, may have great physiological importance for the carbon assimilation of haloarchaea and also for the carbon cycling in hypersaline ecosystems.

In addition, we have also developed an engineered *H. mediterranei* strain with an increase of approximately 20% in PHBV production (Zhao *et al.*, 2013). Therefore, based on our elucidated PHBV biosynthesis pathway and its regulation, *H. mediterranei* has showed great potential to be engineered as a promising archaeal cell factory for future industrial production of PHBV.

Key words: haloarchaea, carbon metabolism, bioplastic production

Acknowledgements

This work was supported by grants from the National 863 Program of China, the National Natural Science Foundation of China, and the Chinese Academy of Sciences.

References

- Cai Lei, Cai Shuangfeng, Zhao Dahe, Wu Jinhua, Wang Lei, Liu Xiaoqing, Li Ming, Hou Jing, Zhou Jian, Liu Jingfang, Han Jing, and Xiang Hua, 2014. Analysis of the transcriptional regulator GlpR, the promoter elements, and the post-transcriptional processing involved in the fructose-induced activation of the phosphoenolpyruvate-dependent sugar phosphotransferase system in *Haloferax mediterranei*. *Applied and Environmental Microbiology*, 80(4): 1430–1440.
- Cai Shuangfeng, Cai Lei, Liu Hailong, Liu Xiaoqing, Han Jing, Zhou Jian, and Xiang Hua, 2012. Identification of the haloarchaeal type phasin (PhaP) that functions in polyhydroxyalkanoate accumulation and granule formation in *Haloferax mediterranei*. *Applied and Environmental Microbiology*, 78(6): 1946–1952.
- Feng Bo, Cai Shuangfeng, Han Jing, Liu Hailong, Zhou Jian, and Xiang Hua, 2010. Identification of the *phaB* genes and analysis of the PHBV precursor supplying pathway in *Haloferax mediterranei*. *Acta Microbiologica Sinica*, 50(10): 1305–1312.
- Han Jing, Hou Jing, Liu Hailong, Cai Shuangfeng, Feng Bo, Zhou Jian, and Xiang Hua, 2010a. Wide distribution among halophilic archaea of a novel polyhydroxyalkanoate synthase subtype with homology to bacterial type III synthases. *Applied and Environmental Microbiology*, 76(23): 7811–7819.
- Han Jing, Hou Jing, Zhang Fan, Ai Guomin, Li Ming, Cai Shuangfeng, Liu Hailong, Wang Lei, Wang Zejian, Zhang Silinag, Cai Lei, Zhao Dahe, Zhou Jian, and Xiang Hua, 2013. Multiple propionyl-CoA supplying pathways for production of bioplastic poly(3-hydroxybutyrate-co-3-hydroxyvalerate) in *Haloferax mediterranei*. *Applied and Environmental Microbiology*, 79(9): 2922–2931.
- Han Jing, Li Ming, Hou Jing, Wu Linping, Zhou Jian, and Xiang Hua, 2010b. Comparison of four *phaC* genes from *Haloferax mediterranei* and their function in different PHBV copolymer biosyntheses in *Haloarcula hispanica*. *Saline Systems*, 6: 9.
- Han Jing, Lu Qiuhe, Zhou Ligang, Liu Hailong, and Xiang Hua, 2009. Identification of the polyhydroxyalkanoate (PHA)-specific acetoacetyl coenzyme A reductase among multiple FabG paralogs in *Haloarcula hispanica* and reconstruction of the PHA biosynthetic pathway in *Haloferax volcanii*. *Applied and Environmental Microbiology*, 75(19): 6168–6175.
- Han Jing, Lu Qiuhe, Zhou Ligang, Zhou Jian, and Xiang Hua, 2007. Molecular characterization of the *phaEC_{Hm}* genes required for biosynthesis of poly(3-hydroxybutyrate) in the extremely halophilic archaeon *Haloarcula marismortui*. *Applied and Environmental Microbiology*, 73(19): 6058–6065.
- Han Jing, Zhang Fan, Hou Jing, Liu Xiaoqing, Li Ming, Liu Hailong, Cai Lei, Zhang Bin, Chen Yaping, Zhou Jian, Hu Songnian, and Xiang Hua, 2012. Complete genome sequence of the metabolically versatile halophilic archaeon *Haloferax mediterranei*, a poly(3-hydroxybutyrate-co-3-hydroxyvalerate) producer. *Journal of Bacteriology*, 194 (16): 4463–4464.
- Hou Jing, Feng Bo, Han Jing, Liu Hailong, Zhao Dahe, Zhou

- Jian, and Xiang Hua, 2013a. Haloarchaeal type β -ketothiolases involved in poly(3-hydroxybutyrate-co- 3-hydroxyvalerate) synthesis in *Haloferax mediterranei*. *Applied and Environmental Microbiology*, 79(17): 5104–5111.
- Hou Jing, Han Jing, Cai Lei, Zhou Jian, LüYang, Jin Cheng, Liu Jingfang, and Xiang Hua, 2013b. Characterization of genes for chitin catabolism in *Haloferax mediterranei*. *Applied Microbiology and Biotechnology*, 98(3): 1185–1194.
- Liu Hailong, Han Jing, Liu Xiaoqing, Zhou Jian, and Xiang Hua, 2011a. Development of *pyrF*-based gene knockout systems for genome-wide manipulation of the archaea *Haloferax mediterranei* and *Haloarcula hispanica*. *Journal of Genetics and Genomics*, 38(6): 261–269.
- Liu Hailong, Luo Yuanming, Han Jing, Wu Jinhua, Wu Zhenfang, Feng Deqin, Cai Shuangfeng, Li Ming, Liu Jingfang, Zhou Jian, and Xiang Hua, 2013. Proteome reference map of *Haloarcula hispanica* and comparative proteomic and transcriptomic analysis of polyhydroxyalkanoate biosynthesis under genetic and environmental perturbations. *Journal of Proteome Research*, 12(3): 1300–1315.
- Liu Hailong, Wu Zhenfang, Li Ming, Zhang Fan, Zheng Huajun, Han Jing, Liu Jingfang, Zhou Jian, Wang Shengyue, and Xiang Hua, 2011b. Complete genome sequence of *Haloarcula hispanica*, a model haloarchaeon for studying genetics, metabolism, and virus-host interaction. *Journal of Bacteriology*, 193(21): 6086–6087.
- Lu Qiuhe, Han Jing, Zhou Ligang, Zhou Jian, and Xiang Hua, 2008. Genetic and biochemical characterization of the poly(3-hydroxybutyrate-co-3-hydroxyvalerate) synthase in *Haloferax mediterranei*. *Journal of Bacteriology*, 190(12): 4173–4180.
- Zhao Dahe, Cai Lei, Wu Jinhua, Li Ming, Liu Hailong, Han Jing, Zhou Jian, and Xiang Hua, 2013. Improving polyhydroxyalkanoate production by knocking out the genes involved in exopolysaccharide biosynthesis in *Haloferax mediterranei*. *Applied Microbiology and Biotechnology*, 97(7): 3027–3036.